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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/522,753

DATE: 03/27/2000
TIME: 16:21:37

Input Set: I522753.RAW

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

Does Not Comply
Corrected Diskette Needed

1 <110> Evans, Ronald M.
2 Chen, J. Don
3 <120> A FAMILY OF TRANSCRIPTIONAL
4 CO-REPRESSORS THAT INTERACT WITH NUCLEAR HORMONE RECEPTORS
5 AND USES THEREFOR
6 <130> SALK1510-3
7 <150> 09/337,384
8 <151> 1999-06-21
9 <150> 08/522,726
10 <151> 1995-09-01
11 <160> 11
12 <170> FastSEQ for Windows Version 4.0

ERRORED SEQUENCES FOLLOW

E--> 13 <210> 6
14 <211> 8388
15 <212> DNA
16 <213> Mus musculus
17 <220>
18 <221> CDS
19 <222> (626)...(8047)
20 <221> misc_feature
21 <222> (1)...(8388)
22 <223> n = A,T,C or G
23 <400> 6
W--> 24 cttaaaaaaa aaacccttac ttgtggttaa aggaaaagaa ataaagactt aggaaaaatg 60
25 taattttcca gggggtacct acacccaaga catatgggttc tcaagaggna ctcagcatat 120
26 cactttgatt ccagagaagc tacaaaagtc attaccaaac tccaggctgg aaagcagtgc 180
27 tcatactaaa tatttaaaca tttaaagacc tgattaagag acatcaaagg ctttatacca 240
28 ggggcacacc aacagagaca ggctttttca aggataattt atgtctgccc attgtcttct 300
29 ggcttaggag acatagaggg aaacatcacc taggaaaacc agtaaccaat gtgtaccatc 360
30 caggagttat tctatgacaa aaccaaaggt tttgttcttg tgtacttctc tgtgcaccat 420
31 ctttctatat ctatttagaa aacaaaacaa attttggtaa cacgcttggtg tataaagagc 480
32 aggacagcgg tgtcacagat caacctagaa agtaattatt taacgagtaa atgactcata 540
33 taggacaagg caagctgtga ctttcaacct gttctgtctc gtgccgaatt cggcagcagc 600
34 caaagcctac ctggacccta ccacc atg tca gga tcc aca cag cct gtg gca 652
35 Met Ser Gly Ser Thr Gln Pro Val Ala
36 1 5
37 cag aca tgg cgg gct gct gag ccc cgc tac cca ccc cat ggc atc tcc 700
38 Gln Thr Trp Arg Ala Ala Glu Pro Arg Tyr Pro Pro His Gly Ile Ser
39 10 15 20 25

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40	tac ccg gtg cag ata gcc cgg tcc cac acg gac gtg ggg ctg ctt gag	748
41	Tyr Pro Val Gln Ile Ala Arg Ser His Thr Asp Val Gly Leu Leu Glu	
42	30 35 40	
43	tac caa cac cac ccc cgt gac tac acc tca cac ctg tca ccc ggt tcc	796
44	Tyr Gln His His Pro Arg Asp Tyr Thr Ser His Leu Ser Pro Gly Ser	
45	45 50 55	
46	atc atc cag cca cag agg agg cgg ccc tca ctg ctg tca gag ttc cag	844
47	Ile Ile Gln Pro Gln Arg Arg Arg Pro Ser Leu Leu Ser Glu Phe Gln	
48	60 65 70	
49	cct ggg agt gaa cgg tct cag gag ctc cac ctg cgc cct gag tcc cgc	892
50	Pro Gly Ser Glu Arg Ser Gln Glu Leu His Leu Arg Pro Glu Ser Arg	
51	75 80 85	
52	acg ttc ctg cct gag ctg ggc aag ccc gac ata gaa ttc acc gag agc	940
53	Thr Phe Leu Pro Glu Leu Gly Lys Pro Asp Ile Glu Phe Thr Glu Ser	
54	90 95 100 105	
55	aag cgc ccc cgc ctg gag cta cta ccc gat acc ctg ctg cgc cca tca	988
56	Lys Arg Pro Arg Leu Glu Leu Leu Pro Asp Thr Leu Leu Arg Pro Ser	
57	110 115 120	
58	ccc ctg ctg gcc act ggg cag ccg agt ggg tct gaa gac ctt acc aag	1036
59	Pro Leu Leu Ala Thr Gly Gln Pro Ser Gly Ser Glu Asp Leu Thr Lys	
60	125 130 135	
61	gac cgt agc ctg gca ggc aag ctg gag cct gtg tca cct ccc agt ccc	1084
62	Asp Arg Ser Leu Ala Gly Lys Leu Glu Pro Val Ser Pro Pro Ser Pro	
63	140 145 150	
64	ccg cac gct gac cct gag cta gag ctg gcg cca tct cga ctg tcc aag	1132
65	Pro His Ala Asp Pro Glu Leu Glu Leu Ala Pro Ser Arg Leu Ser Lys	
66	155 160 165	
67	gag gag ctg atc cag aac atg gac cgc gtg gac cgt gag atc acc atg	1180
68	Glu Glu Leu Ile Gln Asn Met Asp Arg Val Asp Arg Glu Ile Thr Met	
69	170 175 180 185	
70	gta gag cag cag atc tcc aag ctg aag aag aag cag caa cag ttg gag	1228
71	Val Glu Gln Gln Ile Ser Lys Leu Lys Lys Lys Gln Gln Gln Leu Glu	
72	190 195 200	
73	gag gag gcc gcc aag ccg ccc gaa ccc gag aag cct gtg tcg cca cca	1276
74	Glu Glu Ala Ala Lys Pro Pro Glu Pro Glu Lys Pro Val Ser Pro Pro	
75	205 210 215	
76	ccc ata gaa tca aag cac cga agc ctg gtc cag atc atc tac gat gag	1324
77	Pro Ile Glu Ser Lys His Arg Ser Leu Val Gln Ile Ile Tyr Asp Glu	
78	220 225 230	
79	aac cgg aag aaa gcc gaa gcc gca cac cgg atc cta gaa ggc ctg ggg	1372
80	Asn Arg Lys Lys Ala Glu Ala Ala His Arg Ile Leu Glu Gly Leu Gly	
81	235 240 245	
82	ccc cag gtg gag ctg cct ctg tac aac cag ccg tct gac aca cgc cag	1420
83	Pro Gln Val Glu Leu Pro Leu Tyr Asn Gln Pro Ser Asp Thr Arg Gln	
84	250 255 260 265	
85	tac cat gaa aac atc aaa ata aac cag gcg atg cgg aag aag ctg atc	1468
86	Tyr His Glu Asn Ile Lys Ile Asn Gln Ala Met Arg Lys Lys Leu Ile	
87	270 275 280	
88	ttg tac ttt aag cgg agg aac cac gcg cgc aag cag tgg gaa cag cgc	1516
89	Leu Tyr Phe Lys Arg Arg Asn His Ala Arg Lys Gln Trp Glu Gln Arg	

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140	Asn His Glu Lys Glu Ala Val Ala Ser Lys Gly Arg Lys Thr Ala Asn	
141	555 560 565	
142	agc caa ggc cgc cgc aaa ggc cgt atc acg cgc tcc atg gcc aac gag	2380
143	Ser Gln Gly Arg Arg Lys Gly Arg Ile Thr Arg Ser Met Ala Asn Glu	
144	570 575 580 585	
145	gcc aac cat gag gag aca gcc acc cca cag caa agt tca gag ctg gct	2428
146	Ala Asn His Glu Glu Thr Ala Thr Pro Gln Gln Ser Ser Glu Leu Ala	
147	590 595 600	
148	tcc atg gag atg aac gag agt tct cgc tgg act gag gaa gag atg gag	2476
149	Ser Met Glu Met Asn Glu Ser Ser Arg Trp Thr Glu Glu Glu Met Glu	
150	605 610 615	
151	aca gca aag aaa ggc ctc ctg gaa cat ggg agg aac tgg tca gcc att	2524
152	Thr Ala Lys Lys Gly Leu Leu Glu His Gly Arg Asn Trp Ser Ala Ile	
153	620 625 630	
154	gcc cgc atg gtg ggc tcc aag acc gtg tcc cag tgt aag aac ttc tac	2572
155	Ala Arg Met Val Gly Ser Lys Thr Val Ser Gln Cys Lys Asn Phe Tyr	
156	635 640 645	
157	ttc aac tac aag aag agg cag aac ctg gac gaa atc ctt cag cag cac	2620
158	Phe Asn Tyr Lys Lys Arg Gln Asn Leu Asp Glu Ile Leu Gln Gln His	
159	650 655 660 665	
160	aag cta aag atg gag aag gag agg aac gct cgg agg aag aag aag aag	2668
161	Lys Leu Lys Met Glu Lys Glu Arg Asn Ala Arg Arg Lys Lys Lys Lys	
162	670 675 680	
163	acc cca gct gcg gcg agc gag gag aca gcc ttc cca cct gcc gct gag	2716
164	Thr Pro Ala Ala Ala Ser Glu Glu Thr Ala Phe Pro Pro Ala Ala Glu	
165	685 690 695	
166	gac gaa gag atg gaa gca tca ggc gca agt gcc aat gag gaa gag ctg	2764
167	Asp Glu Glu Met Glu Ala Ser Gly Ala Ser Ala Asn Glu Glu Glu Leu	
168	700 705 710	
169	gcg gag gag gca gaa gcc tca cag gcc tct ggg aat gag gtt ccc aga	2812
170	Ala Glu Glu Ala Glu Ala Ser Gln Ala Ser Gly Asn Glu Val Pro Arg	
171	715 720 725	
172	gtt ggg gag tgc agt ggc cca gct gct gtc aac aac agc tct gat act	2860
173	Val Gly Glu Cys Ser Gly Pro Ala Ala Val Asn Asn Ser Ser Asp Thr	
174	730 735 740 745	
175	gag agt gtc cca tcc ccg cgt tca gaa gcc atg aag gac act ggg cct	2908
176	Glu Ser Val Pro Ser Pro Arg Ser Glu Ala Met Lys Asp Thr Gly Pro	
177	750 755 760	
178	aaa ccc act ggc act gaa gca ttg ccc gct gcc acc cag cca cct gtt	2956
179	Lys Pro Thr Gly Thr Glu Ala Leu Pro Ala Ala Thr Gln Pro Pro Val	
180	765 770 775	
181	cct cct cca gaa gaa ccg gca gta gcc cct gct gag ccc tcc cca gtc	3004
182	Pro Pro Pro Glu Glu Pro Ala Val Ala Pro Ala Glu Pro Ser Pro Val	
183	780 785 790	
184	cct gat gcc agt ggc cca cca tcc cca gag cct tcc cat cac ctg ccg	3052
185	Pro Asp Ala Ser Gly Pro Pro Ser Pro Glu Pro Ser His His Leu Pro	
186	795 800 805	
187	cac ccc ccg cta ctg tgg aca agg atg aac aag aag ccc ccg ctg ctc	3100
188	His Pro Arg Leu Leu Trp Thr Arg Met Asn Lys Lys Pro Arg Leu Leu	
189	810 815 820 825	

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190	cag ctc ccc aga cag agg atg cca agg agc aga agt ctg agg ccg agg	3148
191	Gln Leu Pro Arg Gln Arg Met Pro Arg Ser Arg Ser Leu Arg Pro Arg	
192	830 835 840	
193	aga tcg atg tgg gaa aag cca gag gag ccc gag gcc tct gag gag ccc	3196
194	Arg Ser Met Trp Glu Lys Pro Glu Glu Pro Glu Ala Ser Glu Glu Pro	
195	845 850 855	
196	ccg gag agt gta aag agt gac cac aag gag gag acc gag gaa gag cct	3244
197	Pro Glu Ser Val Lys Ser Asp His Lys Glu Glu Thr Glu Glu Glu Pro	
198	860 865 870	
199	gaa gac aaa gcc aag ggc aca gag gcc att gaa act gtg tct gag gca	3292
200	Glu Asp Lys Ala Lys Gly Thr Glu Ala Ile Glu Thr Val Ser Glu Ala	
201	875 880 885	
202	cca ctt aag gtg gag gag gct ggt agc aag gca gct gtg acc aag ggt	3340
203	Pro Leu Lys Val Glu Glu Ala Gly Ser Lys Ala Ala Val Thr Lys Gly	
204	890 895 900 905	
205	tcc agc tca ggt gcc acc cag gac agt gac ttc agt gcc acc tgc agt	3388
206	Ser Ser Ser Gly Ala Thr Gln Asp Ser Asp Phe Ser Ala Thr Cys Ser	
207	910 915 920	
208	gcc gat gag gtg gac gaa ccc gaa gga ggt gac aag ggc agg ctg ctg	3436
209	Ala Asp Glu Val Asp Glu Pro Glu Gly Gly Asp Lys Gly Arg Leu Leu	
210	925 930 935	
211	tca cca agg ccc agc ctc ctc acc ccg gct gga gat ccc cgg gcc agt	3484
212	Ser Pro Arg Pro Ser Leu Leu Thr Pro Ala Gly Asp Pro Arg Ala Ser	
213	940 945 950	
214	acc tcg ccc cag aag ccg ctg gac ctg aag cag ctg aag cag cga gca	3532
215	Thr Ser Pro Gln Lys Pro Leu Asp Leu Lys Gln Leu Lys Gln Arg Ala	
216	955 960 965	
217	gcc gcc atc ccc cct atc cag gtc acc aag gtc cat gag ccc ccc cgg	3580
218	Ala Ala Ile Pro Pro Ile Gln Val Thr Lys Val His Glu Pro Pro Arg	
219	970 975 980 985	
220	gag gac aca gta ccc cca aag cca gtt ccc cct gtg cct cca ccc acg	3628
221	Glu Asp Thr Val Pro Pro Lys Pro Val Pro Pro Val Pro Pro Pro Thr	
222	990 995 1000	
223	cag cac cta cag cca gag ggt gac gtg tct cag cag tcg gga gga agt	3676
224	Gln His Leu Gln Pro Glu Gly Asp Val Ser Gln Gln Ser Gly Gly Ser	
225	1005 1010 1015	
226	cca cgt ggc aag tcc cgc agc cca gtg cct cct gcc gag aaa gag gca	3724
227	Pro Arg Gly Lys Ser Arg Ser Pro Val Pro Pro Ala Glu Lys Glu Ala	
228	1020 1025 1030	
229	gag aaa ccc gca ttc ttt ccg gct ttc cca act gag ggc cca aag cta	3772
230	Glu Lys Pro Ala Phe Phe Pro Ala Phe Pro Thr Glu Gly Pro Lys Leu	
231	1035 1040 1045	
232	ccg act gag ccc cca cgc tgg tca tcg ggc ctg ccc ttc ccc atc cct	3820
233	Pro Thr Glu Pro Pro Arg Trp Ser Ser Gly Leu Pro Phe Pro Ile Pro	
234	1050 1055 1060 1065	
235	cca cgg gag gtg atc aag act tcc cca cac gcc gct gac ccc tct gcc	3868
236	Pro Arg Glu Val Ile Lys Thr Ser Pro His Ala Ala Asp Pro Ser Ala	
237	1070 1075 1080	
238	ttc tcc tac aca ccc ccc ggt cac ccg ctg cct ctg ggc ctc cac gat	3916
239	Phe Ser Tyr Thr Pro Pro Gly His Pro Leu Pro Leu Gly Leu His Asp	

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290	Pro Pro Pro Pro Pro Arg Asp Leu Thr Glu Thr Tyr Lys Pro Arg Pro	
291	1355 1360 1365	
292	ctg gac cct ctg ggt ccc ctg aag ctg aag ccg act cac gag ggt gtg	4780
293	Leu Asp Pro Leu Gly Pro Leu Lys Leu Lys Pro Thr His Glu Gly Val	
294	1370 1375 1380 1385	
295	gta gca act gtg aag gag gcg ggc cgc tct atc cat gag atc ccg aga	4828
296	Val Ala Thr Val Lys Glu Ala Gly Arg Ser Ile His Glu Ile Pro Arg	
297	1390 1395 1400	
298	gag gag ctg cgc cgc aca cct gag cta ccc ctg gca cca cgg cct ctg	4876
299	Glu Glu Leu Arg Arg Thr Pro Glu Leu Pro Leu Ala Pro Arg Pro Leu	
300	1405 1410 1415	
301	aag gag ggt tcc atc acc cag ggc acc cca ctc aag tac gag tct ggg	4924
302	Lys Glu Gly Ser Ile Thr Gln Gly Thr Pro Leu Lys Tyr Asp Ser Gly	
303	1420 1425 1430	
304	gca ccc tcc act ggc acc aag aaa cac gac gtg cgc tcc atc atc ggc	4972
305	Ala Pro Ser Thr Gly Thr Lys Lys His Asp Val Arg Ser Ile Ile Gly	
306	1435 1440 1445	
307	agc ccc ggc cgg cct ttc cct gcc ctg cac ccg ctg gac ata atg gct	5020
308	Ser Pro Gly Arg Pro Phe Pro Ala Leu His Pro Leu Asp Ile Met Ala	
309	1450 1455 1460 1465	
310	gac gcc cgg gca ctg gag cgt gcc tgc tat gaa gag agt ctg aag agc	5068
311	Asp Ala Arg Ala Leu Glu Arg Ala Cys Tyr Glu Glu Ser Leu Lys Ser	
312	1470 1475 1480	
313	cgg tca ggg acc agc agt ggt gca ggg ggc tcc atc aca cgt ggg gct	5116
314	Arg Ser Gly Thr Ser Ser Gly Ala Gly Gly Ser Ile Thr Arg Gly Ala	
315	1485 1490 1495	
316	cca gtc gtc gtg cct gaa ctg ggc aag cca cgg caa agc cca ctg act	5164
317	Pro Val Val Val Pro Glu Leu Gly Lys Pro Arg Gln Ser Pro Leu Thr	
318	1500 1505 1510	
319	tac gaa gac cac ggg gca ccc ttc acc agt cac ctg cca cgt ggc tcc	5212
320	Tyr Glu Asp His Gly Ala Pro Phe Thr Ser His Leu Pro Arg Gly Ser	
321	1515 1520 1525	
322	cct gtg acc acg agg gag ccc acg cca cgc ctt cag gaa ggc agc ctc	5260
323	Pro Val Thr Thr Arg Glu Pro Thr Pro Arg Leu Gln Glu Gly Ser Leu	
324	1530 1535 1540 1545	
325	cta tcc agc aag gcg tcc cag gac cgg aag ctg aca tct aca ccc cgg	5308
326	Leu Ser Ser Lys Ala Ser Gln Asp Arg Lys Leu Thr Ser Thr Pro Arg	
327	1550 1555 1560	
328	gag atc gcc aag tcc cca cac agc act gtg ccc gag cac cac cct cac	5356
329	Glu Ile Ala Lys Ser Pro His Ser Thr Val Pro Glu His His Pro His	
330	1565 1570 1575	
331	ccc atc tcc ccc tat gag cac ttg ctc cgg ggc gtg act ggt gtg gac	5404
332	Pro Ile Ser Pro Tyr Glu His Leu Leu Arg Gly Val Thr Gly Val Asp	
333	1580 1585 1590	
334	ctg tac cgt ggt cac atc cca ttg gcc ttt gac ccc acc tcc ata ccc	5452
335	Leu Tyr Arg Gly His Ile Pro Leu Ala Phe Asp Pro Thr Ser Ile Pro	
336	1595 1600 1605	
337	cga ggg atc cct ctg gaa gca gca gcc gca gcc tac tac ctg ccc cgg	5500
338	Arg Gly Ile Pro Leu Glu Ala Ala Ala Ala Tyr Tyr Leu Pro Arg	
339	1610 1615 1620 1625	

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340	cac ttg gcc ccc agc ccc acc tac cca cac ctg tac cca cct tac ctc	5548
341	His Leu Ala Pro Ser Pro Thr Tyr Pro His Leu Tyr Pro Pro Tyr Leu	
342	1630 1635 1640	
343	atc cgc gcc tac cct gac acg gcg gcc ctg gag aac cgc cag acc atc	5596
344	Ile Arg Gly Tyr Pro Asp Thr Ala Ala Leu Glu Asn Arg Gln Thr Ile	
345	1645 1650 1655	
346	atc aat gac tac atc acc tcg cag cag atg cac cac aac gct gcc tcc	5644
347	Ile Asn Asp Tyr Ile Thr Ser Gln Gln Met His His Asn Ala Ala Ser	
348	1660 1665 1670	
349	gcc atg gcc cag cgt gct gac atg ctg agg ggt ctg tca ccg cga gag	5692
350	Ala Met Ala Gln Arg Ala Asp Met Leu Arg Gly Leu Ser Pro Arg Glu	
351	1675 1680 1685	
352	tcc tcg ctg gcc ctc aat tat gcc gct ggc cca aga ggc att atc gac	5740
353	Ser Ser Leu Ala Leu Asn Tyr Ala Ala Gly Pro Arg Gly Ile Ile Asp	
354	1690 1695 1700 1705	
355	ctg tcc caa gtg cca cac ctg ccc gtg ctg gtg cca cca acg cca ggc	5788
356	Leu Ser Gln Val Pro His Leu Pro Val Leu Val Pro Pro Thr Pro Gly	
357	1710 1715 1720	
358	acc cct gcc acc gcc atc gac cgc ctt gcc tac ctc ccc act gcg ccc	5836
359	Thr Pro Ala Thr Ala Ile Asp Arg Leu Ala Tyr Leu Pro Thr Ala Pro	
360	1725 1730 1735	
361	cca ccc ttc agc agc cgc cac agt agc tca ccg ctg tcc cca gga ggc	5884
362	Pro Pro Phe Ser Ser Arg His Ser Ser Ser Pro Leu Ser Pro Gly Gly	
363	1740 1745 1750	
364	ccc act cac cta gct aaa cca act gcc aca tct tca tcg gag cgg gaa	5932
365	Pro Thr His Leu Ala Lys Pro Thr Ala Thr Ser Ser Ser Glu Arg Glu	
366	1755 1760 1765	
367	cgg gaa cgt gag cgg gaa cga gac aag tcc atc ctc acg tct acc act	5980
368	Arg Glu Arg Glu Arg Glu Arg Asp Lys Ser Ile Leu Thr Ser Thr Thr	
369	1770 1775 1780 1785	
370	aca gtg gag cat gca ccc atc tgg aga cct ggt acg gag cag agc agc	6028
371	Thr Val Glu His Ala Pro Ile Trp Arg Pro Gly Thr Glu Gln Ser Ser	
372	1790 1795 1800	
373	ggg gct ggg gcc agc agc cgc ccc gcc tcc cac acc cac cag cac tcg	6076
374	Gly Ala Gly Gly Ser Ser Arg Pro Ala Ser His Thr His Gln His Ser	
375	1805 1810 1815	
376	ccc atc tcc ccc cgg acc cag gac gcc ttg cag cag agg ccc agt gtg	6124
377	Pro Ile Ser Pro Arg Thr Gln Asp Ala Leu Gln Gln Arg Pro Ser Val	
378	1820 1825 1830	
379	ctg cac aac acg agc atg aag ggc gtg gtc acc tcc gtg gaa ccc ggc	6172
380	Leu His Asn Thr Ser Met Lys Gly Val Val Thr Ser Val Glu Pro Gly	
381	1835 1840 1845	
382	acg ccc acg gtc ctg agg tgg gcc agg tcc acc tcc acc tct tcg cct	6220
383	Thr Pro Thr Val Leu Arg Trp Ala Arg Ser Thr Ser Thr Ser Ser Pro	
384	1850 1855 1860 1865	
385	gtc cgc cca gct gcc aca ttc cca cct gcc acc cac tgc cca ctt ggt	6268
386	Val Arg Pro Ala Ala Thr Phe Pro Pro Ala Thr His Cys Pro Leu Gly	
387	1870 1875 1880	
388	ggc acc ctt gaa ggg gtc tac cct acc ctc atg gag ccc gtc ctg tta	6316
389	Gly Thr Leu Glu Gly Val Tyr Pro Thr Leu Met Glu Pro Val Leu Leu	

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440	Pro His Ser Glu Gly Gly Lys Arg Ser Pro Glu Pro Ser Lys Thr Ser	
441	2155 2160 2165	
442	gtc ctg ggc agc agc gag gat gcc att gag cct gtg tcc cca cca gag	7180
443	Val Leu Gly Ser Ser Glu Asp Ala Ile Glu Pro Val Ser Pro Pro Glu	
444	2170 2175 2180 2185	
445	ggc atg act gag cca gga cat gct cgg agc act gcg tac cca ctg ctg	7228
446	Gly Met Thr Glu Pro Gly His Ala Arg Ser Thr Ala Tyr Pro Leu Leu	
447	2190 2195 2200	
448	tat cga gac ggg gaa cag ggc gag ccc agg atg ggt cta gag tct cca	7276
449	Tyr Arg Asp Gly Glu Gln Gly Glu Pro Arg Met Gly Leu Glu Ser Pro	
450	2205 2210 2215	
451	ggc aac acc agc cag ccg cca acc ttc ttc agt aag ctg act gag agc	7324
452	Gly Asn Thr Ser Gln Pro Pro Thr Phe Phe Ser Lys Leu Thr Glu Ser	
453	2220 2225 2230	
454	aac tcc gcc atg gtg aag tcg aag aag cag gag atc aac aag aaa ctc	7372
455	Asn Ser Ala Met Val Lys Ser Lys Lys Gln Glu Ile Asn Lys Lys Leu	
456	2235 2240 2245	
457	aac acc cac aac cgg aac gag cca gaa tac aat att ggc cag cct ggg	7420
458	Asn Thr His Asn Arg Asn Glu Pro Glu Tyr Asn Ile Gly Gln Pro Gly	
459	2250 2255 2260 2265	
460	acg gaa atc ttc aac atg ccc gcc atc act gga gca ggc ctt atg acc	7468
461	Thr Glu Ile Phe Asn Met Pro Ala Ile Thr Gly Ala Gly Leu Met Thr	
462	2270 2275 2280	
463	tgt aga agc cag gcg gtg caa gaa cac gcc agc acc aac atg ggg cta	7516
464	Cys Arg Ser Gln Ala Val Gln Glu His Ala Ser Thr Asn Met Gly Leu	
465	2285 2290 2295	
466	gag gcc att att aga aag gca ctc atg ggt aaa tat gat cag tgg gaa	7564
467	Glu Ala Ile Ile Arg Lys Ala Leu Met Gly Lys Tyr Asp Gln Trp Glu	
468	2300 2305 2310	
469	gag ccc ccg ccg ctc ggc gcc aat gct ttt aac cct ctg aat gcc agc	7612
470	Glu Pro Pro Pro Leu Gly Ala Asn Ala Phe Asn Pro Leu Asn Ala Ser	
471	2315 2320 2325	
472	gcc agt ctg ccc gct gct gct atg ccc ata acc act gct gac gga cgg	7660
473	Ala Ser Leu Pro Ala Ala Ala Met Pro Ile Thr Thr Ala Asp Gly Arg	
474	2330 2335 2340 2345	
475	agt gac cac gca ctc acc tcg cca ggt gga ggt ggg aaa gcc aag gtc	7708
476	Ser Asp His Ala Leu Thr Ser Pro Gly Gly Gly Lys Ala Lys Val	
477	2350 2355 2360	
478	tct ggc aga cct agc agc cga aaa gcc aag tcg cca gca cca ggc cta	7756
479	Ser Gly Arg Pro Ser Ser Arg Lys Ala Lys Ser Pro Ala Pro Gly Leu	
480	2365 2370 2375	
481	gcg tcc gga gac cga ccc cct tct gtc tcc tca gta cac tca gag ggg	7804
482	Ala Ser Gly Asp Arg Pro Pro Ser Val Ser Ser Val His Ser Glu Gly	
483	2380 2385 2390	
484	gac tgc aat cgc cga aca cca ctc acc aac cgt gtg tgg gag gac cgg	7852
485	Asp Cys Asn Arg Arg Thr Pro Leu Thr Asn Arg Val Trp Glu Asp Arg	
486	2395 2400 2405	
487	ccc tca tct gca ggg tcc acg cca ttc ccc tac aac cct ttg att atg	7900
488	Pro Ser Ser Ala Gly Ser Thr Pro Phe Pro Tyr Asn Pro Leu Ile Met	
489	2410 2415 2420 2425	

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RAW SEQUENCE LISTING
 PATENT APPLICATION US/09/522,753

DATE: 03/27/2000
 TIME: 16:21:37

Input Set: I522753.RAW

490	agg cta cag gca ggt gtc atg gcc tcc ccg ccc cca cct ggc ctt gcg	7948
491	Arg Leu Gln Ala Gly Val Met Ala Ser Pro Pro Pro Pro Gly Leu Ala	
492	2430 2435 2440	
493	gca ggc agc ggg ccc cta gct ggt ccc cac cac gcc tgg gat gag gag	7996
494	Ala Gly Ser Gly Pro Leu Ala Gly Pro His His Ala Trp Asp Glu Glu	
495	2445 2450 2455	
496	ccc aag cca ctg ctg tgt tca cag tat gag aca ctc tcg gac agc gag	8044
497	Pro Lys Pro Leu Leu Cys Ser Gln Tyr Glu Thr Leu Ser Asp Ser Glu	
498	2460 2465 2470	
499	tga ccacggattg ggggggagcg gtgccaggtc ccgcacaagg cagaagcagc	8097
E--> 500	* ccagcatgga gcagacagct gctgactccc gagactgagg aaggagcccc tgagtctgcc	8157
W--> 502	tgcgcgtcca tccgtncgtc gtncaactcat ctgtccatcc agagctggca ttctgcctgt	8217
503	ctaaagcctt aactaagact tccaccccg gctggccctg cgcagtgacc ttacactcag	8277
W--> 504	gggattgttt accttggtgc tcganaaggg ggagtggaca ggaaggggag ggacaagccg	8337
W--> 505	ggccangagg gggggggaca ancaattcgt gtgtcaagtc gcactcntgc t	8388

Input Set: I522753.RAW

Line	Error/Warning	Original Text
14	E Input 8388, Calc# Bases 8389 differ	<211> 8388
25	W "N" or "Xaa" used: Feature required	taattttcca gggggtacct acaccaaga catatggt
500	E Number of Bases conflict w/ Running Total	*
500	E Wrong Nucleic Acid Designator	*
502	W "N" or "Xaa" used: Feature required	tgcgcgtcca tccgtncgtc gtncactcat ctgtccat
504	W "N" or "Xaa" used: Feature required	gggattgttt accttgggtc tcganaaggg ggagtgga
505	W "N" or "Xaa" used: Feature required	ggccangagg gggggggaca ancaattcgt gtgtcaag